

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Tartaglia, Louis A.  
Weng, Xun
- (ii) TITLE OF THE INVENTION: NUCLEIC ACID MOLECULES ENCODING  
GLUTEX AND USES THEREOF
- (iii) NUMBER OF SEQUENCES: 10
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: Fish & Richardson P.C.  
(B) STREET: 225 Franklin Street  
(C) CITY: Boston  
(D) STATE: MA  
(E) COUNTRY: USA  
(F) ZIP: 02110-2804
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Diskette  
(B) COMPUTER: IBM Compatible  
(C) OPERATING SYSTEM: Windows95  
(D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: 09/299,349  
(B) FILING DATE: 26-APR-1999
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: 09/031,392  
(B) FILING DATE: 26-FEB-1998
- (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Meiklejohn, Ph.D., Anita L.  
(B) REGISTRATION NUMBER: 35,283  
(C) REFERENCE/DOCKET NUMBER: 07334/072002
- (ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: 617/542-5070  
(B) TELEFAX: 617/542-8906  
(C) TELEX: 200154

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2343 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:  
(A) NAME/KEY: Coding Sequence  
(B) LOCATION: 73...1761

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TCGACCCACG CGTCCGGCCT TGGCAGAGTC TGGGGTCCCT GGACTGAGCC ATCAGCTGGG	60
TCACTGAGAC CC ATG GCA AGG AAA CAA AAT AGG AAT TCC AAG GAA CTG GGC	111
Met Ala Arg Lys Lys Gln Asn Arg Asn Ser Lys Glu Leu Gly	
1 5 10	
CTA GTT CCC CTC ACA GAT GAC ACC AGC CAC GCC GGG CCT CCA GGG CCA	159
Leu Val Pro Leu Thr Asp Asp Thr Ser His Ala Gly Pro Pro Gly Pro	
15 20 25	
GGG AGG GCA CTG CTG GAG TGT GAC CAC CTG AGG AGT GGG GTG CCA GGT	207
Gly Arg Ala Leu Leu Glu Cys Asp His Leu Arg Ser Gly Val Pro Gly	
30 35 40 45	
GGA AGG AGA AGA AAG GAC TGG TCC TGC TCG CTC CTC GTG GCC TCC CTC	255
Gly Arg Arg Arg Lys Asp Trp Ser Cys Ser Leu Leu Val Ala Ser Leu	
50 55 60	
GCG GGC GCC TTC GGC TCC TCC TTC CTC TAC GGC TAC AAC CTG TCG GTG	303
Ala Gly Ala Phe Gly Ser Ser Phe Leu Tyr Gly Tyr Asn Leu Ser Val	
65 70 75	
GTG AAT GCC CCC ACC CCG TAC ATC AAG GCC TTT TAC AAT GAG TCA TGG	351
Val Asn Ala Pro Thr Pro Tyr Ile Lys Ala Phe Tyr Asn Glu Ser Trp	
80 85 90	
GAA AGA AGG CAT GGA CGT CCA ATA GAC CCA GAC ACT CTG ACT CTG CTC	399
Glu Arg Arg His Gly Arg Pro Ile Asp Pro Asp Thr Leu Thr Leu Leu	
95 100 105	
TGG TCT GTG ACT GTG TCC ATA TTC GCC ATC GGT GGA CTT GTG GGG ACG	447
Trp Ser Val Thr Val Ser Ile Phe Ala Ile Gly Gly Leu Val Gly Thr	
110 115 120 125	
TTA ATT GTG AAG ATG ATT GGA AAG GTT CTT GGG AGG AAG CAC ACT TTG	495
Leu Ile Val Lys Met Ile Gly Lys Val Leu Gly Arg Lys His Thr Leu	
130 135 140	
CTG GCC AAT AAT GGG TTT GCA ATT TCT GCT GCA TTG CTG ATG GCC TGC	543
Leu Ala Asn Asn Gly Phe Ala Ile Ser Ala Ala Leu Leu Met Ala Cys	
145 150 155	
TCG CTC CAG GCA GGA GCC TTT GAA ATG CTC ATT GTG GGA CGC TTC ATC	591
Ser Leu Gln Ala Gly Ala Phe Glu Met Leu Ile Val Gly Arg Phe Ile	
160 165 170	
ATG GGC ATA GAT GGA GGC GTC GCC CTC AGT GTG CTC CCC ATG TAC CTC	639
Met Gly Ile Asp Gly Gly Val Ala Leu Ser Val Leu Pro Met Tyr Leu	
175 180 185	
AGT GAG ATC TCA CCC AAG GAG ATC CGT GGC TCT CTG GGG CAG GTG ACT	687
Ser Glu Ile Ser Pro Lys Glu Ile Arg Gly Ser Leu Gly Gln Val Thr	
190 195 200 205	
GCC ATC TTT ATC TGC ATT GGC GTG TTC ACT GGG CAG CTT CTG GGC CTG	735
Ala Ile Phe Ile Cys Ile Gly Val Phe Thr Gly Gln Leu Leu Gly Leu	
210 215 220	
CCC GAG CTG CTG GGA AAG GAG AGT ACC TGG CCA TAC CTG TTT GGA GTG	783
Pro Glu Leu Leu Gly Lys Glu Ser Thr Trp Pro Tyr Leu Phe Gly Val	
225 230 235	

ATT GTG GTC CCT GCC GTT GTC CAG CTG CTG AGC CTT CCC TTT CTC CCG Ile Val Val Pro Ala Val Val Gln Leu Leu Ser Leu Pro Phe Leu Pro 240 245 250	831
GAC AGC CCA CGC TAC CTG CTC TTG GAG AAG CAC AAC GAG GCA AGA GCT Asp Ser Pro Arg Tyr Leu Leu Leu Glu Lys His Asn Glu Ala Arg Ala 255 260 265	879
GTG AAA GCC TTC CAA ACG TTC TTG GGT AAA GCA GAC GTT TCC CAA GAG Val Lys Ala Phe Gln Thr Phe Leu Gly Lys Ala Asp Val Ser Gln Glu 270 275 280 285	927
GTA GAG GAG GTC CTG GCT GAG AGC CAC GTG CAG AGG AGC ATC CGC CTG Val Glu Glu Val Leu Ala Glu Ser His Val Gln Arg Ser Ile Arg Leu 290 295 300	975
GTG TCC GTG CTG GAG CTG CTG AGA GCT CCC TAC GTC CGC TGG CAG GTG Val Ser Val Leu Glu Leu Leu Arg Ala Pro Tyr Val Arg Trp Gln Val 305 310 315	1023
GTC ACC GTG ATT GTC ACC ATG GCC TGC TAC CAG CTC TGT GGC CTC AAT Val Thr Val Ile Val Thr Met Ala Cys Tyr Gln Leu Cys Gly Leu Asn 320 325 330	1071
GCA ATT TGG TTC TAT ACC AAC AGC ATC TTT GGA AAA GCT GGG ATC CCT Ala Ile Trp Phe Tyr Thr Asn Ser Ile Phe Gly Lys Ala Gly Ile Pro 335 340 345	1119
CCG GCA AAG ATC CCA TAC GTC ACC TTG AGT ACA GGG GGC ATC GAG ACT Pro Ala Lys Ile Pro Tyr Val Thr Leu Ser Thr Gly Gly Ile Glu Thr 350 355 360 365	1167
TTG GCT GCC GTC TTC TCT GGT TTG GTC ATT GAG CAC CTG GGA CGG AGA Leu Ala Ala Val Phe Ser Gly Leu Val Ile Glu His Leu Gly Arg Arg 370 375 380	1215
CCC CTC CTC ATT GGT GGC TTT GGG CTC ATG GGC CTC TTC TTT GGG ACC Pro Leu Leu Ile Gly Gly Phe Gly Leu Met Gly Leu Phe Phe Gly Thr 385 390 395	1263
CTC ACC ATC ACG CTG ACC CTG CAG GAC CAC GCC CCC TGG GTC CCC TAC Leu Thr Ile Thr Leu Thr Leu Gln Asp His Ala Pro Trp Val Pro Tyr 400 405 410	1311
CTG AGT ATC GTG GGC ATT CTG GCC ATC ATC GCC TCT TTC TGC AGT GGG Leu Ser Ile Val Gly Ile Leu Ala Ile Ile Ala Ser Phe Cys Ser Gly 415 420 425	1359
CCA GGT GGC ATC CCG TTC ATC TTG ACT GGT GAG TTC TTC CAG CAA TCT Pro Gly Gly Ile Pro Phe Ile Leu Thr Gly Glu Phe Phe Gln Gln Ser 430 435 440 445	1407
CAG CGG CCG GCT GCC TTC ATC ATT GCA GGC ACC GTC AAC TGG CTC TCC Gln Arg Pro Ala Ala Phe Ile Ile Ala Gly Thr Val Asn Trp Leu Ser 450 455 460	1455
AAC TTT GCT GTT GGG CTC CTC TTC CCA TTC ATT CAG AAA AGT CTG GAC Asn Phe Ala Val Gly Leu Leu Phe Pro Phe Ile Gln Lys Ser Leu Asp 465 470 475	1503